

Outline of Microarray Chip Technology approach

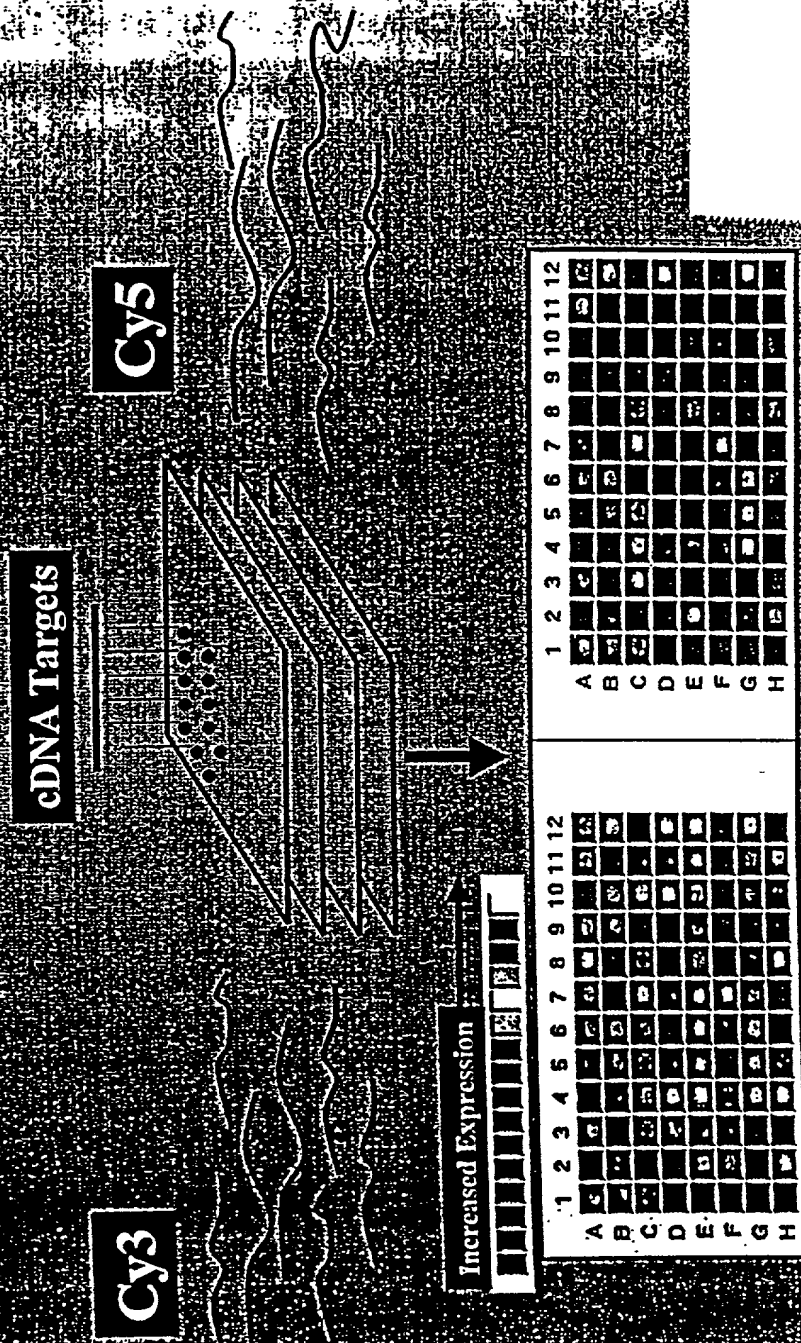


FIG. 1

General protocol for *in vitro* whole gene CD8⁺ T cell priming

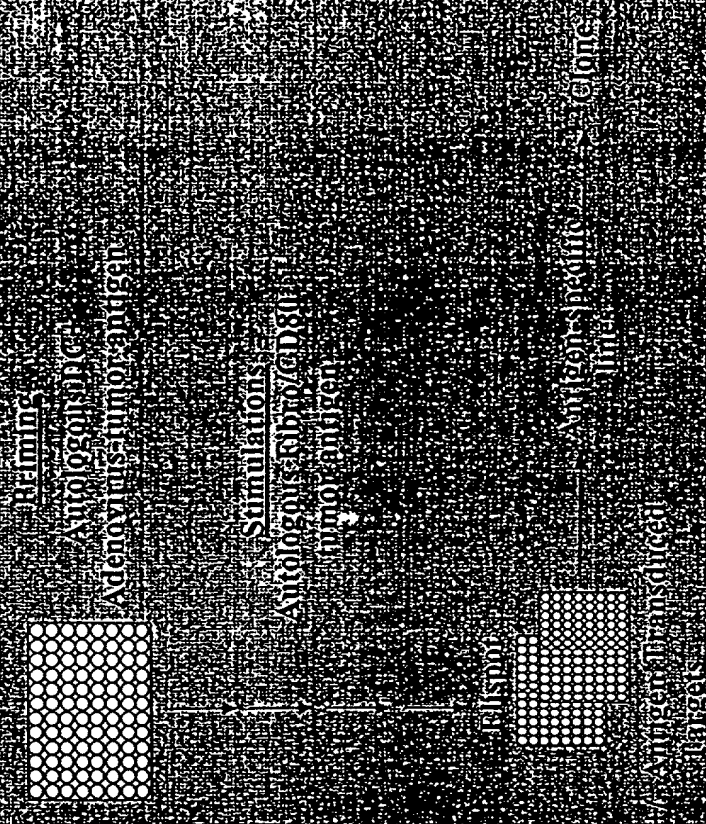


FIG. 2

General protocol for *in-vivo* whole gene CD4⁺ T cell priming

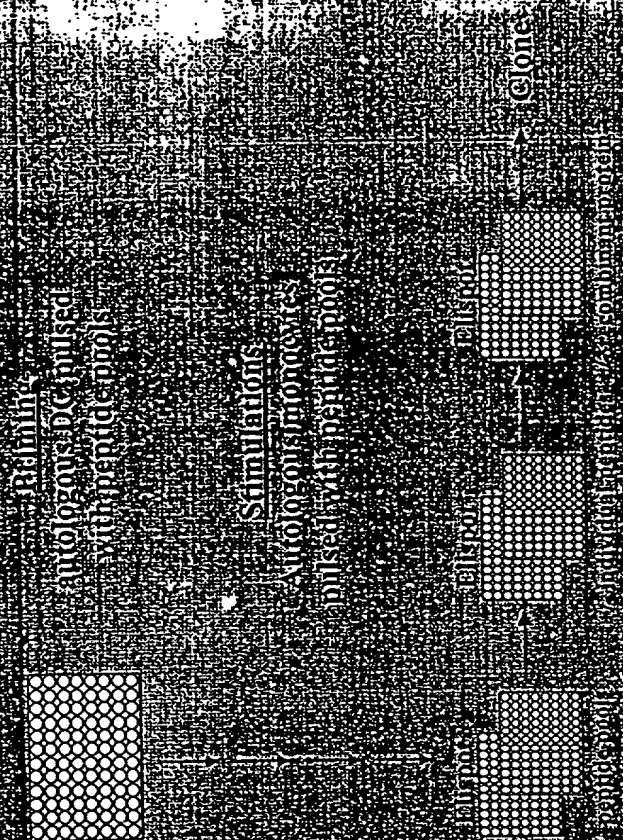


FIG. 3

LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins <small>see RNA 959</small>	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell <small>see RNA 958</small>	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.
 RED: Normal essential tissue probes where gene expression is to be avoided.
 BLACK : Normal tissue probes where gene expression is acceptable.

Figure 4

High Differential Expression in Group 1				All Mean Signal 1 > 0.3		Threshold: 0.3		GenBank Access		GenBank Description		GenSeq		GenSeq		GenSeq	
All Lymphomas > N comparison for Lymphomas				Ratio		Mean		ID		GenBank Description		GenSeq		GenSeq		GenSeq	
Seq. ID	Element (86)	Patent	BP	Ratio	Signal 1	Signal 2	Mean	Mean	GenBank Access	GenBank Description	GenSeq	GenSeq	GenSeq	GenSeq	GenSeq	GenSeq	GenSeq
No. 0.1																	
10,516	R0439 C2	505	334	20.63	1.596	0.077	0.077	0.077	3928244	ig kappa light chain VJ region	14 (891537)	2	0	2	0	34	
10,505	R0432 F1	505	265	14.19	0.338	0.024	0.024	0.024	13591713	ig superfamily receptor translocat. assoc. protein 2c (RTA2)	(20) 12000954	5	0	4	0	2	
10,532	R0458 E10	505	265	8.97	0.532	0.059	0.059	0.059	77053003	hypothetical protein (BM-009)	77 (8266743)	4	0	4	2	3	
10,487	R0408 A10	505/528	289	8.97	0.313	0.035	0.035	0.035	3	ADP-ribosylation factor binding protein GGA2s	63 (12883422)	18	0	12	3	7	
10,534	R0459 D1	505	432	6.79	0.64	0.094	0.094	0.094	25	heat shock protein hsp86	0	1	0	6	0	8	
10,500	R0424 C3	528	486	6.62	0.4	0.06	0.06	0.06	6	cDNA: FLJ22136 fs, clone HEP20890	74 (12798470)	1	0	1	4	1	
10,495	R0417 D10	505	210	5.99	0.571	0.095	0.095	0.095	4	hypothetical protein DKFZP564K0822	111 (12946011)	7	0	7	2	4	
10,535	R0459 E11	519	365	5.89	0.445	0.075	0.075	0.075	3	hypothetical protein DKFZP343B195	38 (7850181)	8	0	11	2	7	
10,504	R0431 C7	505	218	5.76	0.302	0.052	0.052	0.052	1	DNA seq. from clone RP3-437M21 on Chr. 22q13.2-13.33	15 (1275016)	2	0	2	0	1	
10,488	R0408 D7	494	302	4.54	0.355	0.078	0.078	0.078	1	Chr. 16 BAC clone C1987SK-A-735G6, complete	85 (11592124)	3	0	3	2	2	
10,492	R0414 F8	505	528	3.94	0.304	0.077	0.077	0.077	3	Chr. 22q11 clone b461k10, complete seq.	2 (12000954)	6	0	6	0	4	
10,507	R0433 H9	505	456	3.9	0.302	0.077	0.077	0.077	3	ig superfamily receptor translocation-associated 2 (RTA2)	69 (13283950)	4	0	4	4	4	
10,499	R0424 A9	528	528	3.89	0.328	0.084	0.084	0.084	17	protein x 0004 (LOC51184), DKFZP761B1514	81 (11063636)	1	0	2	1	3	
10,498	R0421 F11	528	501	3.75	0.355	0.095	0.095	0.095	3	hypothetical protein DKFZP761B1514 (DKFZP761B1514)	14 (12343165)	5	0	5	0	2	
10,493	R0414 H4	505	637	3.55	0.313	0.088	0.088	0.088	2	mRNA for KIAA1607 protein, partial cds	1 (12070989)	2	0	2	0	2	
10,508	R0436 A3	505	0	3.21	0.308	0.096	0.096	0.096	0	0							
0.1 - 0.2																	
10,525	R0440 F7	505	378	11.05	1.664	0.151	0.151	0.151	160	rearranged ig kappa light chain variable region(L.26)	250 (13547215)	101	0	71	62	40	
10,523	R0440 E2	505	616	10.75	1.555	0.146	0.146	0.146	12	B lymphocyte antigen CD20 (B1, Bp35)	10 (6866994)	1	0	1	2	43	
10,528	R0441 D5	505	279	10.15	1.788	0.176	0.176	0.176	171	rearranged immunoglobulin lambda light chain	2 (12909772)	1	0	1	0	38	
10,517	R0439 C6	505	617	10.15	1.298	0.128	0.128	0.128	12	B lymphocyte antigen CD20	40 (12019778)	3	0	3	0	40	
10,526	R0441 B2	505	616	9.86	1.117	0.113	0.113	0.113	12	B lymphocyte antigen CD20 (B1, Bp35)	7 (11592147)	3	0	3	0	43	
10,497	R0421 C1	528	737	9.68	1.204	0.124	0.124	0.124	0	0	0	15	0	17	0	16	
10,513	R0438 E8	548	364	9.47	1.374	0.145	0.145	0.145	24	MHC class II DP4v3-alpha-1 chain	16 (12902627)	6	0	1	0	39	
10,524	R0440 F2	505	431	8.25	1.537	0.186	0.186	0.186	11	B lymphocyte antigen CD20 (B1, Bp35)	9 (8155824)	4	0	5	1	35	
10,522	R0440 E1	505	222	7.71	1.29	0.167	0.167	0.167	165	germline (GLV3S2 gene for ig lambda variable region	1 (1471308)	5	0	5	0	40	
10,527	R0441 C4	505	576	6.84	1.131	0.165	0.165	0.165	12	B lymphocyte antigen CD20 (B1, Bp35)	20 (10162753)	1	0	2	1	1	
10,533	R0459 A7	505	645	6.19	0.826	0.133	0.133	0.133	3	cDNA FLJ20706 fs, clone KAI1273	8 (565914)	1	0	2	1	1	
10,530	R0459 C12	548	475	5.5	0.731	0.133	0.133	0.133	3	cDNA: FLJ22747 fs, clone KAI1A0120	0	8	0	9	0	9	
10,496	R0421 A3	528	595	5.23	0.984	0.188	0.188	0.188	0	0	0	7	0	7	0	15	
10,520	R0440 C6	505	259	4.45	0.73	0.164	0.164	0.164	6	B lymphocyte antigen CD20	38 (11593303)	3	0	2	2	2	
10,509	R0437 B3	505	730	4.04	0.646	0.18	0.18	0.18	2	DNA seq. from clone RP11-29716 on Chr. 13, complete seq.	6 (5886479)	1	0	1	0	4	
10,519	R0440 C3	505	456	3.91	0.41	0.105	0.105	0.105	3	ig superfamily receptor translocation-associated 2 (RTA2)	27 (1933024)	14	0	9	0	8	
10,491	R0410 A9	505	315	3.88	0.738	0.19	0.19	0.19	0	0	213 (13456724)	27	1	24	7	12	
10,489	R0408 H9	516	562	3.66	0.374	0.102	0.102	0.102	12	KIAA0101 gene product (KIAA0101), mRNA	67 (10817681)	27	0	25	0	6	
10,494	R0416 G9	505	545	3.64	0.472	0.13	0.13	0.13	7	cDNA: FLJ22139 fs, clone HEP20959	162 (13284392)	25	0	17	5	12	
10,486	R0407 B5	516	524	3.43	0.592	0.173	0.173	0.173	12	KIAA0101 gene product (KIAA0101), mRNA	38 (5924697)	1	0	1	0	1	
10,503	R0428 D3	528	399	3.24	0.428	0.132	0.132	0.132	1	M. musculus adult male oocum cDNA, RIKEN full-length cDNA	31 (6892642)	2	0	2	0	5	
10,521	R0440 D11	528/505	603	3.21	0.485	0.151	0.151	0.151	0	0	66 (12883422)	18	0	12	3	7	
10,490	R0409 D9	505/528	289	3.11	0.366	0.118	0.118	0.118	4	ADP-ribosylation factor binding protein GGA2s	13 (10035232)	1	0	1	1	1	
10,511	R0437 G11	505	526	3.03	0.439	0.145	0.145	0.145	3	hypothetical protein MGCT1314	1 (2889816)	1	0	1	0	16	
0.2																	
10,518	R0439 G12	505	485	5.76	3.324	0.577	0.577	0.577	11	B lymphocyte antigen CD20	233 (13442196)	111	0	104	56	3	
10,515	R0439 A8	505	293	4.7	6.398	1.362	1.362	1.362	222	rearranged immunoglobulin lambda light chain	59 (1191101)	3	0	3	1	1	
10,501	R0425 A3	528	512	4.33	1.01	0.234	0.234	0.234	0	0	126 (8168503)	2	0	3	1	128	
10,529	R0458 B8	548	678	4.32	1.394	0.323	0.323	0.323	1	clone O14b03 Myo26 protein mRNA	232 (12341574)	226	0	211	41	15	
10,531	R0458 C6	505	251	4.31	1.744	0.405	0.405	0.405	201	rearranged immunoglobulin lambda light chain	1 (6638748)	1	0	1	0	54	
10,512	R0438 E3	505	295	4.29	2.147	0.5	0.5	0.5	6	B-lymphocyte cell-surface antigen B1 (CD20)	0	1	0	3	0	39	
10,536	R0459 E12	528	507	4.24	0.978	0.231	0.231	0.231	7	proteoglycan 1, secretory granule (PRG1)	13 (12770918)	3	0	3	0	4	
10,510	R0437 D8	494	510	4.21	7.328	1.74	1.74	1.74	11	B lymphocyte antigen CD20	51 (7044121)	6	0	7	0	4	
10,506	R0433 F4	505	420	3.65	0.81	0.222	0.222	0.222	99	immunoglobulin lambda joining 3 (IGLJ3)	100 (14069888)	103	0	102	56	123	
10,514	R0438 F7	528	200	3.44	6.874	2.001	2.001	2.001	0	0	0	3	0	3	0	3	
10,502	R0425 A5	528	433	3.33	0.766	0.23	0.23	0.23	0	0	0	3	0	3	0	3	

Figure 5

Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank Description		Genbank Accession		Genbank 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Figure 6

Hematology therapeutic Ab candidates

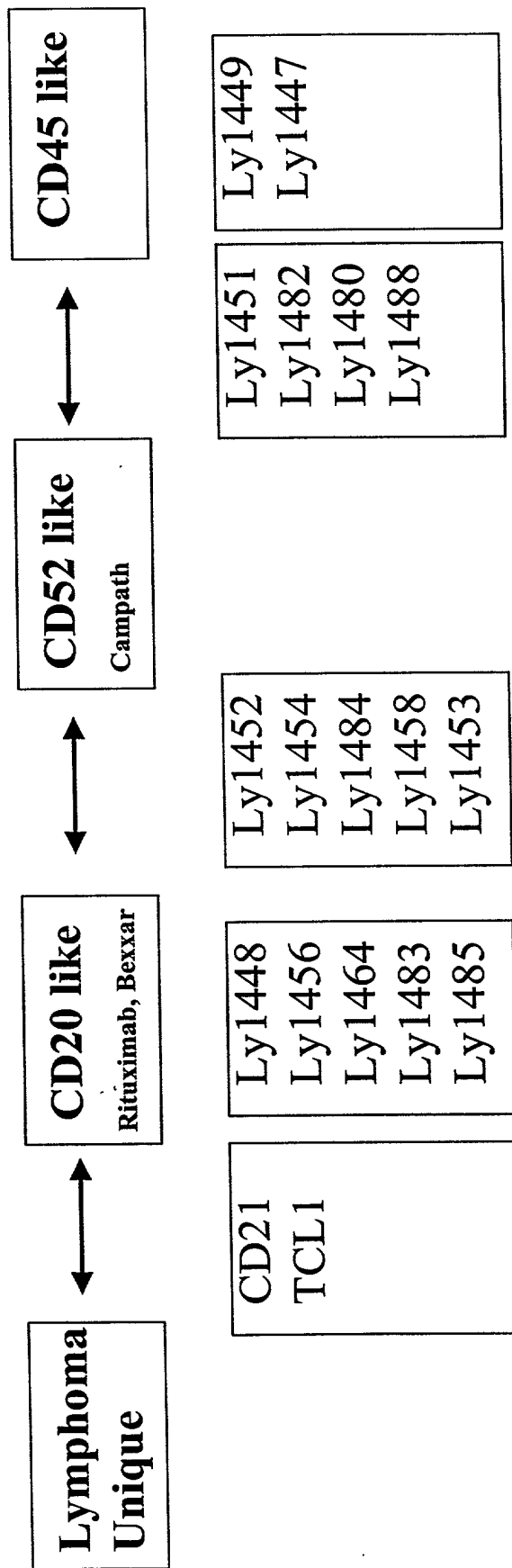


Figure 7

Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

Gene	CD34+	CD19+	CD14+	CD2+	Ly	Hodgkin	Myeloma	CLL*	AML
CD20	-	+++	-	-	+++	+	+	++	+/-
CD21	-	+	-	-	+++	++	+	+	-
TCL1	-	+	-	-	+++	+	-	++	-
Ly1448	-	+++	-	-	+++		++	++	-
Ly1452	-	+++	-	-	+++	+	+	++++	+/-
Ly1456	-	++	-	+	++ T-NHL	+	++	++++	-
Ly1464	-	+++	-	-	+++	+	n.d.	n.d.	n.d.
Ly1483	-	+++	-	+	+++	++	+	n.d.	-
Ly1458	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1481P	-	+++	-	+	+++	+	n.d.	n.d.	n.d.
Ly1485P	-	+++	-	-	++	-	n.d.	n.d.	n.d.
Ly1480	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1488	+	++	++	+	+++	+	n.d.	n.d.	n.d.
Ly1484	+	++	+/-	+/-	+++	++	n.d.	n.d.	n.d.
Ly1482	++	+++	++	+++	+++	++	n.d.	n.d.	n.d.
Ly1453	++	++	++	++	+++ T-NHL	+++	+++	+++	+++
Ly1449	++	+	-	-	+	+	+	+++	++
Ly1447	++	+++	+	+	++	++	n.d.	n.d.	n.d.
Ly1451	++	++	-	-	++	+	+	++	++++
CD52	++	+++	++	++	++	++	n.d.	++	n.d.
CD45	+++	+++	+++	+++	+++		n.d.	n.d.	n.d.

* single probe

Figure 8

SEQ ID NO:
10,581

Lyl447 sequence:
CCTTCAACGACTGGAGTGGGGTCCACCCACATTAGGGTGGAGTTTGTCTGCCACTGTGCAGTTATCATTCTGGGATGGG
GGTACCTTACTCTCCCAATGAGAAATTCTAAATTTCTCTTTTGTAGCCTGGTGCCTCCACCTTCTCANAACATGCATAGGG
CGTGAGCTTTGTTGGTGATGTGACCTCCAGAACAGACTGTGAGCAGATTTTTTTCTTAATCCTGAGCCTATGCTTGCTG
CTGTCTCTTCTTGACTTTCAACTAGGCCCTAAAAAAGCGN

SEQ ID NO:
10,582

Lyl448 Sequence
CCAGGGTTAGGACATTCAAATGTCTTTATCCACATTCCTGAAGGATAATTGTTATAGATTCCCTACCTCCATAGGAATGC
TTATAATGGATTATCTATACATCTCCACATTCCACATTTTGCATTAGAGAATGGAATCAGTCAAACCTGTTCACAGA
GTTTCCCTTAGAGTTCTCACCTGTTGTCTTATATCCATCTAGGAATCCCCATCTCTAATGTAAGCTTGGAGATCCGGGCC
CCCGGGGACAGGTGACTGAAGGACAAAACTGATCCTGCTCTGCTCAGTGGCTGGGGGTACAGGAAATGTCACATTCTC
CTGGTACAGAGAGGCCACAGGAACAGTATGGGAAAGAAAAACCCAGCGTTCCCTGTGAGCAGAGCTGGAGATCCAGCTG
TGAAAGAGAGTGATGCCGGCAAATATTACTGTAGAGCTGACACAGGCCCATGTGCCTATCCAGAGCAAGGTGGTGAATATC
CCTGTGAGAAGACCTGATGGCTATAGAAGAGACCTCATGACAG

SEQ ID NO:
10,583

Lyl449 Sequence
CCACATTGGGAATTTGACACACAGGTGCCTGCTCCACCANNACAGAGAGGCTCAGGAGATTGTCCAGGGACAAGGAGACCT
GGCCGGACCTCTGCAGGGAGGTGAGGCCCTGCCCCCATCTTGTCCCATCACATTCTGGATGTTTGGCATCCCCAGGCTC
CTGGGAGGGGAGAAGTGCTGATAAAAGGCCAAAAATCACACAGAAAGAACAGAAAACTCCACGCATCTCCTACATAG
GTGCTACCGTATTCTACGAGCACGGGGCTGTGTTGAAGACTCCCTCTGGAAGTTACAGAAGGAAGCCCAAGAGTTT
AGCCTCACAGCCTCTTTCTCAGATGCAGTACCACCTTACCAAACCTTGGCACATCCAACCACTCCTTTTCATAATTTTACA
CCTGTTTGTGGCCTGGCTGACAGATATTTGTNATTGATCTTTCTAATTTTCAAGGATTCTAAATGTGTTTGGAGATCTG
GTCAGCACTCANGGATTCTGTCTTT

SEQ ID NO:
10,584

Lyl451 Sequence
CTGCTGCTAAATACCTNTGAGAACTCTGCTTCTATCTAAGGGGACCTACTTTTNTCNGGAATCTCAATACTTGGAAACAA
GAACCTCCTANACGGACCCCTTTGGCATAATGAATTGGACCACTGTAGGTTCCAGGACTAGAGAGCCAGCAATGCCTCCA
TGAACAATCTCACCAATTACTCTGCTCAGGAAACGAGGTAAGTATGACAGCCGAGGCAGCCCTTAGCGCGCTTAGG

SEQ ID NO:
10,585

Lyl452 Sequence
AAAAACCAATAGCAGCCAAAACAGAACATTTGTAACAAAACCAACTATCAGCCCTGTGCTTAAACACAGAATCTGC
ATTCTTTTGAACATTAGTATATGCAATAAAGAGAAATATAGACCATCTTTTCTTAATATACAATACCAATATCTAA
AACAAATGTCAACAATAATAGACACAAATCGGTGTTATCATAGGCATGTTGAACAGTCTTTTTCACAGTACTCAGGGGCA
TCATGGGGCTGCAGAGGCCACACTTTCCAGAAGTTTTCTCCTCGCTGTGATCCTCGCACACCGGGGGCACTCGGAGGACT
GGAAGCACTGTTTGTGAAGCAAGCCCTGACCGCTGAACATCTTCTACATGTTGCTGTCTGAAATGGGAAGATGACAGTC
GTATTCTGGCAAAATTCACAAATAAAGCCCTTCTTGTGACACAGCTCACAGCCAGCCACATGTGCAAGGGAAGCTTGNAG
AATGTCCTTGAGTAAGGGTGCCAGAGCCCTTCTTGTGATCCTGACCAGGTCTCAAGGGAGAACAGGTGGAGCTCATCAG
TCAAGTGTCCCGGCCCTGCCCTACAAACTCCTTTAATGCACTGTTAGCAAACCTACAGGTCTTCAACAGCTTCTTGATAT
GGAAGAGCTGCTCCTGAATTTCTCTC

SEQ ID NO:
10,586

Lyl453 Sequence
CCAAAACTTCAGCATAAAACTATCCTGTCTGTGATTATATATATTTATTACNNNATTTAATAAAACAAAACCACTTT
TGAACCAAGTAATTTTATCTAGTGTGAAAAGAAATTAATCATAGTGTCTATAGTGGCTAGTGCTCTCTAAAAGTAGACA
TTAAATATTTTATAAATGGAGGGAATCTTTGGAGATTAGTGGCATCTAATCTTGGGGCCTCAGACCCCAAAATCTATA
TATTGACCAAGTGAAGTTGATGATTTGTTATCAAATTTCAAAGCACCTAATGGAACCCCACTTCTCTGTGAAGATT
TTCAGTNCCTTTACAGTTATTTGAAATTTATTTCAATTTCTGTGGAGCCACTTCAGAACTCCAATGGGCCCTTTGCAATATT
AAAATGTGGAGAATGCATTAATCATTATTTAATCAATGATTT

SEQ ID NO:
10,587

Lyl454 Sequence
CCTCTCCACAGGCTGCTTGAGTGTCTCATGACACAACAGTTGGCTTACTCCAGAGTGAGCAACTCAAGAGAGAGCAAGG
CAGAAGCTACCAATCTTTATGTTTGAAGTCATGCACCATCTTTTCCAGAGTATCCTGTTGATTATTTTGATCAGCTTG
TTCAGTCTGGGAGGGAATTGCACAAGGGCATGAATACTCACTGGCAAGGATCATTTGGGGGCCATCTTGAAGCTGTGTG
AATGAGCAAAATGAATGCACAGATAGAATATTAGCAGTGACATGATGCTAGAGGTACCTACCCCACTGTCTCTGTGCTC
TTCTCCCCCAACCTCCCTGCTCCAGGCAAGAAGCCCTCTAGCCCTGCTTGATCACTTTCAAGCACTCAACATCTTCA
GGGAACCTATTCCGCGTGGGACAGTGTAAATTAGTGGAAAACCTTTTTCAAAAGTTGAAATCAGTTCTCTGTGTCTA
TTACCTGCTGATCACTGTCCAGACTTCTGGAGGACACAGAGCAAGTTTATTCTCTTACTGATGGTAGCCTTTGAGATC
CATCCCTTCCCTCCAGTATATTAGAGTTACGTAAATTTCTAAAATGCTTAGCAGCTCATTATCTCTGAACA

SEQ ID NO:
10,588

Lyl456 Sequence
AAAGACATGAAAAATATCCCAAGATCATACTAGATCATAATAGCAATTCCTTTACAAATGAATTATGGAGGTAACATGATC
TCTAACAGTTTCTCTCATGTTGTTTAAATGACACAAGGGCAGAGGATCTGCCGACCCCTTGGAACCAAGCGTGAGCTAACCA
GTGCTATAGACACTTCTATGGTGTGCTACCCAGGGAAGTCAAAGCGCTTTGCTCCCTCACTGTCTGTGAGTCTCTCAGCCAT
TAGTAGCCCAACCCCGCTGCTCCAAACTTGTAGTTGTTTCAAATGTTTCTCACTGTTCTCTCTNACTGACCCCACTC
CAGAAAGCCTGGAGAGAGGCCAAGATGCCACCCACCTTCCCAATCCCTCGCCACAGATCTGTGTCTATCAACACTGTG
TAAGTGCCCTTTGCTTCTTCCCTCTTGAAGAGACTGAGAACACACATTTTAAACATGTTTANGAAAATGGGGCAGGCTAA
AAAATGACTGATCCACCGCCAGTGACTCA

SEQ ID NO:
10,589

Lyl458 Sequence
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GGGTTANAATCAAANAACATANAGTNGGGCAATATACTTATCTTACCCATCCCAACCAATCTTACTTACTCATNTC
ATTCTCATTAATTTTGGGAAANCATNANAANATGGGTTCTGTTAGTAANANATTAANAANAATAGCTTTTGTATCCCTG
CCAACACCCCATGCCCCAGGGGGGNCACCCCTCAATACAATAACATGCCAGGAANAGTAAGNTGCCCTTTCTGANGCCGNA
ATCTGCCATCATNTTCCATNTTCCAGNCTNTTCCATGTCNAGNCACAATCTGGGTCTCAGGGATNATACCCGGTCTTA

G

SEQ ID NO:
10,590

Ly1464 Sequence
aaagagaactaatggaagtggattgaatacacagcagctctcaactgggggcaattttgcccc
ccagaggacattgggcaatgtttgagacattttggtcattataacttggggggtggggg
atggtgggatgtgtg

SEQ ID NO:
10,591

Ly1480 Sequence
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ACAGGCAGGGCTGGCTGATAGGGAGTATGGGAGAAGGACACGCTCAGATGAAAAATGTCATGCAACGATTTTCACCACTG
AACACACTGTTTTCTGTGATAGAACTGTCCGCCCTGCTGGGGGACAAAGATATTCACGGCCTCACTAGCCAGTGAGATGC
CACCAGGCGGCCCTGCCCTGATGCTCCTTTGTTACCTGTCTAAAGAAGGACCATAAGGTAAAGGCACCTTACCTTATGG
AGTGAGCCAGACCCAGGGAAGCTTGGGTAGAACAAATCCAAGGGGACGCTGGGTGTGAGAATCCAGCCCAAGCTAG
CTGCTCTAGAAGCCTGGAGG

SEQ ID NO:
10,592

Ly1482 Sequence
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CTAAATATACGATTCTTTGGCATATTGGAATTGGTCAGCCCTCAAAGACCGGCTGGCTACATCGTCGCACGAGACAGTCCC
GCTTATTCTCTGTCACGGACTCGGAGACGGTCTCAGCGGGAGGAGCTCAGGTCTCCTGGGGCCAGACAGTGCCCCAGA
GAGTCCCCAGAAGCATGGACAGTTCTGCTCTGTTTCCATCGCTCAGGCAGGGGAGAGAGTCCGTGG

SEQ ID NO:
10,593

Ly1483 Sequence
GCTGGAGCTTCACTGTGAGTCCCTGAGAGGCTCCTTCCCGATCCTGTACTGGTTTTATCACGAGGATGACACCTTGGGGA
ACATCTCGGCCCCACTCTGGAGGAGGGGATCCTTCAACCTCTCTCTGACTACAGAACATTCTGGAACTACTCATGTGAG
GCTTGACAATGGCCTGGGGGCCAGCACAGTAAAGTGGTGACACTCAATGTTACAGGAACCTCCAGGAACAGAACAGGCC
TTACCRCTGCGGGAATCAGGGGGCTGGTGSTCARCATCYTCGTCCTTGYWGTGCTGCTGCTCTGCTGCATTACGCCAGG
GCCGAAGGAAACCAGGAGGACTTCTGCCACTGGAACATCTAGTCACAGTCTAGTGAGTGTGAGGAGCCTTCTCGTC
CAGG

SEQ ID NO:
10,594

Ly1484 Sequence
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ATCGGCCATGGAGAGGGTTGGGCTGCAGAGCTGTGATTGCCAGAGGCCCTTCTTGGAACTGTGGGGAAGGAGGCCCTG
GGGGTTTCTTCTGTAGGCGAGGCTCAGGCCCCAGTCACCTCTGCCACCCTCAGCCTGGCACTGTTGTGCCAGAGCCTCTG
CTGCCTCTCTCTCCTACCCATCTGCAGACCAGCAGAAATATTCTCCCCCTCTCATCACCACAGGAGTTTGGTGTGGTT
TCTGGACACGGCCAGAGCAGGTCACTGCGGGGCTGGTTTTGCTGGGCTTCCCTGTCAAAGCAATGCTAACGTCCAGCTCT
CGACTCAAGGCCAGGTTCTTCTCCCACTTGTGGCCTCTTGGGCTTGGAGGCTGAGCCAGGGGCTCCTCTCCTGCTGGCCG
TCCAGGAACAGGACATCTTACATCCTCAGTCTTCCAAACCCGACCATGCCGTCTTGACTCCCGGTGATGATGATCTGG
CTTGTGTCCCATGCTGGGCCCTCCATCAGGCAGCAACAGGTTATGGCTCCTTCTGGGCCCCAGGCTGTGGTGTGCTGG

SEQ ID NO:
10,595

Ly1485
CTGTCTCCACTGTGGAGTTACTATTTTCTCTTTTCCCCATTTTATTCATCAGAAGCCAGTCACTAAGCGAGGTCAAATC
CAGGACAGGGGAATTAAGTGCCACCTTCTGGAGAGGGAGCATTACATTTATTACTTGGGATCCTTCTGTAAGGAAGAGC
TGTTTTCTCCTCTAAAAAACTCTTTAATCCTTTTAAGCCTCAATTTCTTAATTGTGAAATGGGGCTAATACCTGTATCCAA
CCAAGGGAGTAGTTAGAAGGTAACATGATAGGTGGAAGCACTTAACATAGGCAAAATGTTATTATCAGGAATGATCGAG
AGACCCATCCAATCTCTGAAGGAGTCACTTAACCTCTACTGTACTGCAAGCGCTGTAAAGTCTTGATCTTTTCACTGGGG
GTAAAGGCCCCAGTCCCTGAGACGGGCCAGTTTGAAGACAGGCTGGTTTTTCTCTGTTCTCCTGAGAGCCCTTCAGA
TGAGAAGGGAGGCTGGAGACAGAATGCCAAAAGCCCATTAAGGACAGGCCTTGCAATTTAGAGAGGGAGCAGGTCTAG
AGAAGAACCAGAGGAGCTCAG

SEQ ID NO:
10,596

Ly1488
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AAACAGTCCAGGATGGAACCTGGTTTACCCCTTCATACCAGCTCCAAGCCCCAKACCATGGGAGCTGTCTGGGATGTTGAT
CCTTGAGAACTTGGCCCTGTGCTTTAGACCCAAGGACCCGATTCTGGGCTAGGAAAGAGAGAACAAAGCAAGCCGGGGCT
ACCTGCCCCAGGTGG

Figure 1a. Lyl1464 full length DNA sequence (SEQ ID NO: 10,597)

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1 gatgcaagga gatgagacag ttaaatttac ttcctctttt ctaatctgag aggtttcatg
61 ttgaagaaaa tcagtgttgg ggttgacagga gacctaaaca cagtcacccat gaagctgggc
121 tgtgtcctca tggcctgggc cctctacctt tcccttggtg tgctctgggt ggcccagatg
181 ctactggctg ccagttttga gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc
241 agctgccaca cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc
301 tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat cctccaaggt
361 ccagccaagc cagtttttga aggggacctg ctggttctgc gctgccaggc ctggcaagac
421 tggccactga ctcaggtgac cttctaccga gatggctcag ctctgggtcc cccggggcct
481 aacagggaat tctccatcac cgtggtacaa aaggcagaca gcgggcacta ccaactgcagt
541 ggcatcttcc agagccctgg tcctgggatc ccagaaacag catctgttgt ggctatcaca
601 gtccaagaag tgtttccagc gccaatctc agagctgtac cctcagctga accccaagca
661 ggaagcccca tgacctgag ttgtcagaca aagttgcccc tgcaaggttc agctgcccgc
721 ctctcttctt ctttctacaa ggatggaagg atagtcaaaa gcagggggct ctctcagaa
781 ttccagatcc ccacagcttc agaagatcac tccgggtcat actggtgtga ggcagccact
841 gaggacaacc aagtttgaa acagagcccc cagctagaga tcagagtga ggtgcttcc
901 agctctgctg cacctcccac attgaatcca gctcctcaga aatcagctgc tccaggaact
961 gctcctgagg aggcctctgg gcctctgcct ccgcccacaa ccccatcttc tgaggatcca
1021 ggcttttctt ctcctctggg gatgccagat cctcatctgt atcaccagat gggccttctt
1081 ctcaaacaca tgcaggatgt gagagtcttc ctcggtcacc tgctcatgga gttgagggaa
1141 ttatctggcc accggaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt
1201 catccatgat ctcacttaac caccocaata aatctgattc tttattttct cttcctgtcc
1261 tgcacatatg cataagtact tttaacagtt gtcccagttt tttgttagaa taatgtagtt
1321 aggtgagttg aaataaaatt atataaagtg agaattagag tttagctata attgtgtatt
1381 ctctcttaac acaacagaat tctgctgtct agatcaggaa tttctatctg ttatatcgac
1441 cagaatgttg tgatttaaaag agaactaatg gaagtggatt gaatacagca gtctcaactg
1501 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt ggtcattata
1561 cttggggggt tgggggatgg tgggatgtgt gtgctactgg catccagtaa atagaagcca
1621 ggggtgccgc taaacatcct ataatgcaca gggcagttac ccacaacgaa aaataatctg
1681 gcccataatg tcagttgtac tgagtttgag aaacccagc ctaatgaaac cctaggtgtt
1741 gggctctgga atgggacttt gtcccttcta attattatct ctttccagcc tcattcagct
1801 attcttactg acataaccagt ctttagctgg tgctatggtc tgttctttag ttctagtttg
1861 tatccctcca aaagccatta tgttgaaatc ctaatcccca aggtgatggc attaagaagt
1921 gggcctttgg gaagtgatta gatcaggagt gcagagccct catgattagg attagtgcct
1981 ttatttaaaa agggcccca gagctaactc accctccac catatgagga cgtggcaaga
2041 agatgacatg tatgagaacc aaaaacagc tgtcgccaaa caccgactct gtcgttgctt
2101 tgatcttgaa cttccagcct ccagaactat gagaaataaa attctgttgt ttgt

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Figure 1b. Lyl1464 protein sequence (SEQ ID NO: 10,598)

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MKLGCVLMAWALYLSGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVKAYTFSEPPHLIVSYDWLILQGPAPKV
FEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGNREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFFAPILRAVP
SAEPQAGSPMTLSCQTKLPLQSAARLLFSFYKDGRIQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSA
APPTLNPAPQKSAAPGTAPEEAPGLPPPTPSSSEDPGFSSPLGMPDPHLYHQMGLLLKHMVDVRVLLGHLMLRELSGHRKPGTTKA
TAE

```

Figure 10

TMpred Report for Ly1464

Date:

SEQ ID NO: 10,598

MKLGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESSCHTED
DLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQ
AWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSP
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQR
SAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVW
KQSPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPS
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRK
PGTTKATAE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains

Transmembrane Domain 1: 3 - 24 Score: 1.5484

Transmembrane Domain 2: 71 - 92 Score: 1.3009

Transmembrane Domain 3: 158 - 179 Score: 1.3027

Figure 11

20221029 14:50:01

Ly 1464 MHC class binding peptides (SEQID NOs: 10,599-10,819)

Ly1464 A1 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3	FSEPFHLIV	67	67.5
4	LTDAREAGF	52	25
5	SSEDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFQIPTA	222	2.7
8	MPDPHLYHQ	312	2.5
9	LMELRELSG	339	2.25
10	HTEDDLTDA	47	2.25
11	CTEESCHT	40	2.25
12	ALGPPGPNR	118	2
13	LGMPDPHLY	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	1
16	LRELSGHRK	342	0.9
17	QLEIRVQGA	255	0.9
18	WCEAATEDN	239	0.9
19	SAEPQAGSP	179	0.9
20	AREAGFQVK	55	0.9

Ly1464 HLA A2 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLVV	13	4047
2	LLLKHMQDV	323	1006
3	VLMAWALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILOGPAKPV	81	118.2
7	LLGHLLMEL	334	83.53
8	LLAASFETL	25	33.81
9	WQDWPLTQV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916

Ly1464 A3 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLILQGPAK	79	30
2	ELFPAPILR	167	18
3	ALGPPGPNR	118	9
4	VLWVAQMLL	18	6
5	VLMAWALYL	6	5.4
6	LLKHMQDVR	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSCQTK	187	2
9	LLGHLLMEL	334	1.8
10	GMPDPHLYH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35

14	ALYLSLGVL	11	1.35
15	YLSLGVLWV	13	1.2
16	ATEDNQVWK	243	1
17	HMQDVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KAYTFSEPF	63	0.9
20	KQSPQLEIR	251	0.81

Ly1464 A11 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	1
2	WLILQGPAK	79	0.6
3	KQSPQLEIR	251	0.36
4	CQTKLPLQR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPQK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLKHMQDVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKEGTTK	347	0.06
13	RVQGASSSA	259	0.06
14	LPLQRSAAR	196	0.06
15	EFSITVVQK	127	0.06
16	YTFSEPFHL	65	0.06
17	ITVQELFPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKDGR	206	0.04

Ly1464 A24 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLLL	317	200
2	VFEGDLLVL	89	30
3	TFYRDGSAL	111	20
4	GFQVKAYTF	59	15
5	KPVFEGDLL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVLW	12	9
9	IFQSPGPGI	146	7.5
10	APEEAPGPL	285	7.2
11	TFSEPFHLI	66	7.2
12	HLLMELREL	337	6.6
13	MTLSCQTKL	188	6.6
14	VLMAWALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8
20	DVRVLLGHL	330	4.8

Ly1464 A68 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSGHR	341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8
9	VVAITVQEL	160	8
10	WVAQMLLAA	20	8

11	GVLWVAQML	17	8
12	KQSPQLEIR	251	7.5
13	PTLNPAPQK	270	6
14	AVPSAEPQA	176	6
15	ETASVVAIT	156	6
16	VVQKADSGH	132	6
17	WLILQGPAK	79	6
18	LLKHMQDVR	324	5
19	CQTKLPLQR	192	5
20	RVQGASSA	259	4

Ly1464 B7 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	200
2	KPVFEGDLL	87	80
3	APEEAPGPL	285	72
4	LQSAARLL	198	40
5	QVWKQSPQL	248	20
6	VVAITVQEL	160	20
7	IVSYDWLIL	74	20
8	GVLWVAQML	17	20
9	VLMAWALYL	6	12
10	MAWALYLSL	8	12
11	ALYLSLGVL	11	12
12	HMQDVRVLL	327	6
13	APGTAPEEA	281	6
14	SPMTLSCQT	186	6
15	DAREAGFQV	54	6
16	RVLLGHLLM	332	5
17	HLLMELREL	337	4
18	LLGHLLMEL	334	4
19	VLWVAQMLL	18	4
20	HLYHQMGLL	316	4

Ly1464 B8 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	8
2	DAREAGFQV	54	7.2
3	LQSAARLL	198	1.2
4	FSFYKDGR	207	1
5	GCVLMAWAL	4	0.8
6	MAWALYLSL	8	0.8
7	LLGHLLMEL	334	0.4
8	HLYHQMGLL	316	0.4
9	VLMAWALYL	6	0.4
10	AARLLFSFY	202	0.4
11	APILRAVPS	171	0.4
12	ALYLSLGVL	11	0.4
13	HLIVSYDWL	72	0.4
14	LLAASFETL	25	0.4
15	VLWVAQMLL	18	0.4
16	HMQDVRVLL	327	0.3
17	APEEAPGPL	285	0.24
18	LSGHRKPGT	345	0.2
19	GVLWVAQML	17	0.2
20	SSSAAPPTL	264	0.2

Ly1464 B27 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LRELSGHRK	342	2000
2	VRVLLGHLL	331	2000
3	ARLLFSFYK	203	2000
4	AREAGFQVK	55	2000
5	QSAARLLF	199	1000

6	GRIVQSRGL	213	600
7	NREFSITVV	125	600
8	KQSPQLEIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	CQAWQDWPL	99	200
12	LRCQAWQDW	97	200
13	HLYHQMGLL	316	150
14	ALYLSLGVL	11	150
15	VLWVAQMLL	18	150
16	CQTKLPLQR	192	100
17	VQKADSGHY	133	100
18	LQGPAPKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Ly1464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHLIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNREF	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APEEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCQTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
20	DAREAGFQV	54	3.6

Ly1464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTQVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKA	56	18
5	EAGFQVKAY	57	13.5
6	LGMPDPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELFPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDAREA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHLIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPVCTEE	35	1.8

Figure 12
Page 4 of 4

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1464~1.TXT

Beginning with residue: 1 and ending with residue: 359

AMPHI Window size: 11

A - AMPHI mid points of blocks.

R - Residues matching the Rothbard/Taylor motif.

D - Residues matching the IAd motif.

d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MKLGCVLMAWALYLSLGVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREA
GFQVKAYTFSEPFHLIV

.....AAAAAAA...
.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....
.....

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
SYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQ
KADSGHYHCSGIFQSP

.....AA.....AAAAAAA.....AAAAAAA
R.....RRRR..
.....
.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSARLLFSFYK
DGRIVQSRGLSSEF

AAAAAAAAA.....AAAAAAA.....
.....RRRR.....RRRR.....RRRR.....RRRR.....
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD..
.....

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
QIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSAAPTLPAPQKSAAPG
TAPEEAPGPLPPPPTPS

.....AAAAA.....
.....RRRRR.....RRRRR.....
.....DDDDDDDD.....
.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKATA
E

.....AAA.....AAAAA.....AAAAAAAAAAAAA.....
.....RRRR..RRRR.....RRRRRRRRRR.....RRRR....
.....DDDDDD.....
.....

Table 4. Immunogenic portions of Ly1464 (SEQ ID NOs: 10,820-10,842)

MKLGCVLMAWALYLSLGVLWVAQMLLAASF
 LGVLWVAQMLLAASFETLQCEGPVCTEESS
 ETLQCEGPVCTEESSCHTEDDLTDAREAGF

 CHTEDDLTDAREAGFQVKAYTFSEPFHLIV
 QVKAYTFSEPFHLIVSYDWLILQGPAPKPVF
 SYDWLILQGPAPKPVFEGDLLVLRCAWQDW
 EGDLLVLRCAWQDWPLTQVTFYRDGSALG
 PLTQVTFYRDGSALGPPGPNREFSITVVQK
 PPGPNREFSITVVQKADSGHYHCSGIFQSP
 ADSGHYHCSGIFQSPGPGIPETASVVAITV
 GPGIPETASVVAITVQELFPAPILRAVPSA
 QELFPAPILRAVPSAEPQAGSPMTLSCQTK
 EPQAGSPMTLSCQTKLPLQRSAARLLFSFY
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 QIPTASEDHSGSYWCEAATEDNQVWKQSPQ
 EAATEDNQVWKQSPQLEIRVQGASSAAPP
 LEIRVQGASSAAPPPTLNPAPQKSAAPGTA
 TLNPAPQKSAAPGTAPEEAPGPLPPPPTPS
 PEEAPGPLPPPPTPSSEDPGFSSPLGMPDP
 SEDPGFSSPLGMPDPHLYHQMGLLLKHMQD

 HLYHQMGLLLKHMQDVRVLLGHLLMELREL
 VRVLLGHLLMELRELSGHRKPGTTKATAE

Figure 14

10057475.01202

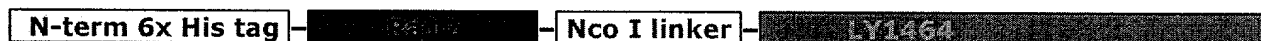
LY1464 and recombinant Ra12-LY1464

Researcher: Alex Gaiger, Aijun Wang, Jonathan Clapper

Reference: cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

Description: LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, **Ra12-LY1464**, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction screening.

Protein Diagram of Ra12-LY1464



Cloning Strategy:

Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and LY1464-antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separated on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 **Ra12-LY1464**. This ligation mixture was used to transform competent E. coli Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant **Ra12-LY1464** in E. coli.

Cloning Primers:

LY1464-sense

5' - CGTCCATGGACatgaagctgggctgtgtcctc - 3' (SEQ ID NO: 10,843)
 prime 21bp 57%GC 56C Tm
 full length 32bp 59%GC 68C Tm

LY1464-antisense

5' - CCTTCTCGAGctatttcagcagtagcctttgtggtc - 3' (SEQ ID NO: 10,844)
 prime 25bp 48%GC 58C Tm
 full length 35bp 51%GC 67C Tm

Protein Expression:

Various E. coli strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For **Ra12-LY1464**, The most optimal expression condition is pCRX2 **Ra12-LY1464** in Tuner (DE3) CodonPlus-RP grown in **2xYS** media at 37°C induced with **1.0mM IPTG** at **25°C** (room temp) for **3hr**.

DNA/Protein Sequence:**LY1464 (DNA) 1080bp (SEQ ID NO: 10,445)**

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Ra12-LY1464 (DNA) 1500bp (SEQ ID NO: 10,467)

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gctgaatag

Ra12-LY1464 (protein) (SEQ ID NO: 10,468)

MHHHHHTAASDNFQLSQGGQGFAIPIGQAMAIAGQIKLPTVHIGPTAFLGLGVVDNNGNGARVQRVVGSA
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LGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVKAYTFSEPFHL
IVSYDWLILQGPAPKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCS
GIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRI
VQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWVKQSPQLEIRVQGASSSAAPPTLNPAPOKSAAPGTAP
EEAPGPLPPPTPSSSEDPGFSSPLGMPDPHLYHQMLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKAT
AE.

Protein Info:**Ra12.LY1464**

Molecular Weight 53010.15 Daltons

499 Amino Acids

29 Strongly Basic(+) Amino Acids (K,R)

46 Strongly Acidic(-) Amino Acids (D,E)

174 Hydrophobic Amino Acids (A,I,L,F,W,V)

128 Polar Amino Acids (N,C,Q,S,T,Y)

5.663 Isoelectric Point

-14.119 Charge at PH 7.0

1484
LyH448. DNA Sequence (SEQ ID NO: 10,846)

```

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Figure 17
Page 1 of 2

10057475-012202

4081 attacacatg actcacctta ttaagggtta ttgcactgaa aaaaaaaaaa agatgggtcg
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Ly1484. Protein sequence (long) (SEQ ID NO: 10,847)

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SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTC
NDYMQYPVPFPWVLADYTTSETLNLANKIFRDLSKPMGAQTKERKLKFIQR
FKEVEKTEGDMTVQCHYYTHYSSAIIIVASYLVRMPPTQAFALQGGSF
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ
DGTVLGDVQLPPWADGDPKRFISLHRKALESDFVSANLHHWIDLIFGYKQ
QGPAAVDAVNI FHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
TKPHPARTAAGKPLPGKDVSTPVSLPGHPQPPFFYSLQSLRPSQVTVKDMY
LFLSGSES PKGAIGHIVSTEKTI LAVERNKVLLPPLWNRTFSWGFDDFSC
CLGSYGSDKVLMTFENLAANGRC LCAVCPSPTTIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGHQAVTCLAASVTFSLLVSGSQDCTCILWDL DHL
THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
EEPLAQPPSPRGHKWEKNLALSREL DVSIALTGKPSKTS PAVTALAVSRN
HTKLLVGD DERGRIFCWSADG

Ly1484. Protein sequence (short) (SEQ ID NO: 10,848)

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVPFPWVLADYTTSETLNL
ANKIFRDLSKPMGAQTKERKLKFIQR FKEVEKTEGDMTVQCHYYTHYSS
AIIIVASYLVRMPPTQAFALQGGSFVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKRFIS
LHRKALESDFVSANLHHWIDLIFGYKQ QGPAAVDAVNI FHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPPFFYSLQSLRPSQVTVKDMYLFLSGSES PKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAANGRC
LCAVCPSPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHQAVT
LAASVTFSLLVSGSQDCTCILWDL DHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALS
ELDVSIALTGKPSKTS PAVTALAVSRNHTKLLVGD DERGRIFCWSADG

a. TMpred Report for Ly1484 Long

Date:

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
TQKLVEKLYSGMFSADPRHILLFILEHIMVVIETASSQRDVLSTLYSSL
NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
HCLLLLNNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEVTPLWE
ETMLKAWQHYLASEKKSASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
HKESQDKNDHISQTNAEQDELTLREAEGEPDEVGVDCTQLTFFPALHES
LHSEDFLELCRERQVILQELLDEKVKTKFSLVIVQGHVSEGVLFFGHQ
HFYICENFTLSPTGDVYCTRHCLSNISDPFIFNLCSKDRSTDHYSQCCHS
YADMRELRLQARFLLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCFQ
SLKKGATSEDTLNLRRYPGSDRIMLQKWQKRDINFEYLMYLNTAAGRTC
NDYMQYPVPVFWVLADYTTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQ
RKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPFFTQAFCALQGGSF
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ
DGTVLGQVQLPPWADGDPKRFISLHRKALESDFVSANLHHWIDLIFGYKQ
QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNGVQVQKLF
TKPHPARTAAGKPLPGKDVSTPVSLPGHPQPFYSLQSLRPSQVTVKDMY
LFSLGSESPKGAIGHIVSTEKTI LAVERNKVLLPPLWNRTFSWGFDFFSC
CLGSYGSDKVLMTFENLAAGRC LCAVCPSPTTIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGHQAVTCLAASVTFSLLVSGSQDCTCILWDLHL
THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
GPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
EEPLAQPPSPRGHKWEKNLALSRELDSIALTGKPSKTSAPVATALAVSRN
HTKLLVGDERGRIFCWSADG (SEQ ID NO: 10587)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1484 Long has 1269 amino acids and 5 Transmembrane Domains

Transmembrane Domain 1:	63 - 84	Score: 1.36675
Transmembrane Domain 2:	118 - 139	Score: 1.38695
Transmembrane Domain 3:	480 - 501	Score: 1.36185
Transmembrane Domain 4:	562 - 583	Score: 1.31785
Transmembrane Domain 5:	725 - 746	Score: 1.3521

b. TMpred Report for Ly1484 (short)

MLQKWQKRDINFEYLMYLNTAAGRTCNDYMQYPVPVFWVLADYTTSETLNL
ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVRMPFFTQAFCALQGGSFVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGQVQLPPWADGDPKRFIS
LHRKALESDFVSANLHHWIDLIFGYKQOGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNGVQVQKLFQTKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTI
LAVERNKVLLPPLWNRTFSWGFDFFSCCLGSYGSDKVLMTFENLAAGRC
LCAVCPSPTTIVTSGTSTVVCVWELSM TKGRPRGLRLRQALYGHQAVTCL
LAASVTFSLLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALS
ELDSIALTGKPSKTSAPVATALAVSRNHTKLLVGDERGRIFCWSADG (SEQ ID NO: 10584)

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Lyl484 has 646 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 102 - 123 Score: 1.3521

Table2a: Ly1484 long MHC class I binding peptides

(SEQID NOs: 10,849-10,906)

HLA A2:

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	FLLCIMHCL	145	836.3
2	YLPEFLTNC	783	818.9
3	KLYSGMFSA	57	742.3
4	FILEHIMV	73	629.3
5	TLYSSLNKV	95	511.9
6	FLQEHWDVV	127	448
7	ILWDLHLT	1093	431.1
8	ALQGGSFVD	743	403.4
9	MQYPVFPWV	654	400.9
10	ALYGHQAQV	1063	222.6
11	YLVRMPFFT	730	188.5
12	CLMHCLLLL	148	181.8
13	GLLSILGFL	120	130
14	VLMTFENLA	1010	118.7
15	ILAVERNKV	973	118.2
16	YLASEKKS	260	98.27
17	ELTPEFFYL	776	97.11
18	YLMYLNTAA	638	84.56
19	ILLFILEHI	70	73.96
20	LLQDIALEI	563	72.72

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KLMPGRQAK	292	135
2	VLLPPLWNR	981	60.75
3	CLGSYGSDK	1001	60
4	KVILYCLSK	102	54
5	CVWELSMK	1044	30
6	LLFGHQHFY	495	30
7	PLWEETMLK	247	30
8	FLSPNEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFYNNDR	580	18
11	KLYSGMFSA	57	13.5
12	GLRLRQALY	1057	12
13	NLANPKIFR	672	12
14	RVWKTEDVK	1183	10
15	QVPKQLFTK	894	9
16	RMPPFTQAF	733	9
17	KLKFIQRFK	694	9
18	RIMLQKWQK	622	9
19	VILQELLDK	465	9
20	IMLQKWQKR	623	6

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	655	300
2	FYICENFTL	502	300
3	TYNSNISFL	138	300
4	NYRRRGQEL	315	264
5	DYTSETLNL	665	200
6	SVLVRMPFF	729	150
7	RYPGSDRIM	616	75
8	RFLLQDIAL	561	60
9	LYSSLNKVI	96	60
10	YYTHYSSAI	717	50
11	FFPALHESL	443	36
12	NFGQVPKQL	891	28
13	SYGSDKVLM	1004	25
14	GFDDFSCCL	994	24
15	EFFYLPEFL	780	24
16	YFYGDRMDL	865	20
17	SFCSFQPSL	594	20
18	RGLRLRQAL	1056	17.28
19	RGQELYASL	319	17.28
20	KNLALSREL	1217	15.84

Figure 19

CID1096 Table 2b.Ly1484 short MHC class I binding peptides

(SEQ ID NOs: 10,909-10,968)

A2

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLPEFLTNC	160	818.9
2	ILWDLHLT	470	431.1
3	ALQGSFDV	120	403.4
4	MQYPVFPWV	31	400.9
5	ALYGHQAV	440	222.6
6	YLVRMPPFT	107	188.5
7	VLMTFENLA	387	118.7
8	ILAVERNKV	350	118.2
9	ELTPEFFYL	153	97.11
10	YLMYLNATA	15	84.56
11	VLADYTSET	39	51.94
12	RMFHSVKST	131	45.8
13	SNFEYIMYL	11	26.76
14	KVLMTFENL	386	22.54
15	LLPPLWNR	359	21.54
16	QLFTKHPHA	275	18.38
17	GAHLSLWNV	507	16.66
18	WDLHLTHV	472	15.5
19	FISLHRKAL	198	13.51
20	CILWDLHL	469	12.25

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	VLLPPLWNR	358	60.75
2	CLGSYGSDK	378	60
3	CWELSMTK	421	30
4	GLRLRQALY	434	12
5	NLANPKIFR	49	12
6	RVWKTEDVK	560	10
7	QVPKQLFTK	271	9
8	RMPPFTQAF	110	9
9	KLKFIQRFK	71	9
10	TILGFVSNF	261	4.05
11	SLPGHPQPF	301	3
12	WIDLIFGYK	218	2.7
13	NLHHWIDLI	214	2.7
14	YMQYPVFPW	30	2.7
15	ELTPEFFYL	153	2.43
16	ALYGHQAV	440	1.5
17	YLPEFLTNC	160	1.35
18	IIVASYLVR	102	1.2
19	DMTVQCHYY	87	1.2
20	QLFTKHPHA	275	1

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	32	300
2	DYTSETLNL	42	200
3	SYLVRMPPF	106	150
4	YYTHYSSAI	94	50
5	NFGQVPKQL	268	28
6	SYGSDKVL	381	25
7	GFDDFSCCL	371	24
8	EFFYLPEFL	157	24
9	YFYGDRMDL	242	20
10	RGLRLRQAL	433	17.28
11	KNLALSREL	594	15.84
12	KVLMTFENL	386	14.4
13	TFSWGFDFF	367	12
14	FYLPEFLT	159	10.8
15	ANPKIFRDL	51	10.08
16	SFDVADRMF	125	10
17	KTSPAVTAL	614	9.6
18	KGRPRGLRL	429	9.6
19	RNKVLLPPL	355	9.6
20	EYLMYLNATA	14	9

Figure 20

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-1.TXT
Beginning with residue: 1 and ending with residue: 1270
AMPHI Window size: 11

A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCFQKLVEKLYSGMFSADPRHILLFIL
.....AAAAA.....AAAA.AAA.....AAAAAAAAA.....
.....RRRRR.....RRRRRRRRRR.....RRRRRRRRRRRRRR.....
.....DDDDDD.....
.....
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
EHIMVVIETASSQRDTVLSTLYSSLNKKVILYCLSKPQOSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
.....AAAAA.....AAAAAAAAAAAAAAAAAAAAAAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....DDDDDD.....DDDDDDDD.....
.....
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSQVHNIQKTVQTLWQQLVAQRQQTLED
.....AAAAA.....AAAAAAAAAAAAAAAAA.....
.....RRRR.....RRRR.....R
.....
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
AFKIDLSVKPGEREVKIEVTPLEWETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPPGRQAK
.....AAAAA.....AAAAA.....AAAAA.....
RRR.....RRRRRRRRRRRRRR.....RRRRR.....
.....
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDFVSCIENYRRRGQELYASLYKHVQRRKCGNIKAANAWARIQEQFLGELGLWSQGEETKPCSPWELD
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRR.....RRRR.....
.....
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WREGPARMRKRIRKLSPLSALSSGRHKESQDKNDHISQTNENQDELTLREAGEPEDEVGVDCTQTLFFPALHES
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRRR.....
.....DDDDDD.....DDDDDDDD.....
.....
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHVSEGVLLFGHQHFYICENFTLSPTGDVYCTRHLN
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRRR.....RRRRR.....
.....
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPFIFNLCSKDRSTDHYSQCHSYADMRELQARFLLQDIALEIFPHNGYSKFLVFYNNDRSKAFKSFCSFQP
A.AAAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRRRRRRRRRRRRRR.....RRRR.....
.....
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNLAAGRTCNQYQYVFPVWLADYTSSETLNLN
.....AAAAA.....AAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRRR.....RRRRR.....
.....DDDDDD.....
.....
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKIFRDLSPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSSAIIVASVLRMPPTQAFQALQGGSF
AAAAA.....AAAAA.....AAAAA.....AAAAA.....
.....RRRR.....RRRRR.....RRRRR.....RRRRR.....R

10057475.012202

.....DDDDDDDDDD.....
.....ddd.....
755 760 765 770 775 780 785 790 795 800 805 810 815 820 825
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPKRFISLH
AAAAAAAAAAAA.AA.AAAA.AAAAAA.....AAAAA.....AAA.....
RRRRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....
.....
830 835 840 845 850 855 860 865 870 875 880 885 890 895 900
RKALESDFVSANLHHWIDLIFGYKQOGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
.....AAAAA.....AAAAAAAAAAAAA.....AAAAA.....AAAAAAAAAAAAAAAAAAAA
RRRRR.RRRR.....RRRRRRR.....RRRR.....RRRR.....
.....DDDDDD.....
.....
905 910 915 920 925 930 935 940 945 950 955 960 965 970 975
TKPHPARTAAGKPLPGKDVSTPVSLLPGHPQFFYSLSLRPSQVTVKDMLFSLGSESPKGAIGHIVSTEKTLA
.....AAAAA.....AAAAA.....
RRRRR.....RRRRRRR.....
DDDDDD.....DDDDDD.....DDDDDD.....
.....
980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050
VERNKVLLPLWNRTFSWGFDDFSCCLGSYGSKVMTFENLAAWGRCLCAVCPSPTTIVTSGTSTVVCVWELSM
.....AAAAA.....
RRRR.....RRRRR.....
DDDDDDDDDDDD.....DDD
.....
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
TKGRPRGLRLRQALYGHQTQAVTCLAASVTFSLLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSGTI
.....AAAAA.....AAA.....AAAA
RRRRRRR.....RRR
DDD.....DDDDDD.....DDDDDDDDDD.....DDDDDD.....DDDD
.ddddddddd.....
.....
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
VSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
A.....AAA.....AAAAA.....
RR.....RRRR.....RRRRRRR.....
D.....DDDDDD.....DDDDDD.....DDDDDD.....
.....
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRRR.....
DDDDDDDD.....DDDDDDDD.....
.....

Figure 21
Page 2 of 2

ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MLQKWQRDISNFEYLMYLNTAAGRTCNQYQVFPVWLADYTSETLNLANPKIFRDLSPKPMGAQTKERKLKFI
AAA.....AAAAA.....AAAAA.....AAA
.....RRRR.....RRRRRRRR.....RRRR.....RRR
.....dddd..
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
ORFKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPTQAFQALQGGSFVADRMFHSVKSTWESASRENMSD
AAAAA.....AAAAA.....AAAAA.....AA.AAAA..AA
R.....RRRR.RRRRR.....RRRRRRRR.....
.....DDDDDDDDDD..
155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPFFYLPEFLTNCNGVEFGCMQDGTVLGDLPPWADGDPKFIHLRKALESDFVSANLHHWIDLIFGY
AAAA.....AAAAA.....AAA.....AAAAA.....
.....RRRR.....RRRR.....RRRR.....RRRR.....RRRRRRRR..
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQGGPAADVAVNIHFHYFYGDRMDLSSITDPLIKSTILGFVSFNGQVQKQLFTKPHPARTAAGKPLPGKDVSTPV
AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAA
.....RRRR.....RRRR.....RRRR.....RRRR.....RRRRRRRR..
.....DDDDDD.....DDDDDD.....DDDD
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPQFFYSLSLRPSQVTVKDMYLSLGSSEPKGAIGHIVSTETILAVERNKVLLPPLWNRTFSWGFDDF
AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAA
.....RRRRRRRR.....RRRR.....RRRR.....
D.....DDDDDD..
380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYSGDKVLMTFENLAAGWRCCLCAVCPPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHQTQAVTC
AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAA
.....RRRR.....DDDDDDDDDD.....DDDDDD.....DDDDDD.....DDD
.....dddddadd..
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTFSLLVSGSQDCTCILWDLHLTHVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNQPLASITT
AAAAA.....AAA.....AAAAA.....AAA..
.....RRRRRR.....RRRR.....RRRR.....RRRRRRRR..
DDDDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
.....AAAAA.....AAAAA.....AAAAA.....AAAAA.....AAAA
.....RRRR.....RRRRRRRR.....RRRRRRRR.....RRRRRRRR..
D.....DDDDDD.....DDDDDD..
605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSPTAVTALAVSRNHTKLLVGDGRGRIFCWSADG
.....RRRRRR.....RRRRRR.....RRRRRR.....RRRRRR.....RRRRRR..
DDDDDDDD.....DDDDDDDD.....DDDDDDDD.....DDDDDDDD.....ddddd

Figure 22

Ly1456P LifeSeqGold Clone Distribution

Ly1456P LifeSeq Gold Search

LifeSeq Template	E Value of hit	Length (bp)	Libraries Found in		Clone Abundance		ORFs * (>50aa)	TMpred **
			Total #	Hemic & Immune #	Total Clone Count	Hemic & Immune		
238330_1	0	1442	55	21	78	33	294bp 177bp 252bp 198bp	No No No No

* = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).
 ** = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred.

ORF#1 = 379>672 = 294bp = 98aa
 ORF#2 = 555>734 = 177bp = 59aa
 ORF#3 = 1037>1291 = 252bp = 84aa
 ORF#4 = 1074>1274 = 198bp = 66aa

Figure 23

```

1  gtcttctccc tgtgtcttca cgtgggtcccc gctgtctgtg cgtgtgtgcc tgatctctc
61  ttcttataag gaccccaatc atattggatt agagcccatc cacaggacct aaatttttcc
121  ctttaactctt ttctctgtttg ccccaagaac actcaccagc agctcttgcg gctgcagcgt
181  ttaccccaaa gtaatttggg cacaacaacat ctccctttta ttattttcac ttgcttttag
241  tgatcaactc ttggaacaa aagacatcat tctacgtata agacatcatt ctagggtatag
301  cgttctgtct ttagtagtgg catttccatt tagaaaatat agtaattctc gatcgctgaa
361  aatgtcaaat ccgagaaaac atagcattcc tatgtgatca ttctcaaga gttgttggcc
421  aaagattcat ttgattaatc ctatttttct gaaatagacg attctgatga ttgagatgat
481  ttgtagtcta gttctgttta cacataactc caagaacagt ttttaatttt tactttcaca
541  ttgaaatca gtcagggttg tttatgtaaa attaaatgag ctctggccaa gcacggtggc
601  tcatgcttat aatcccagca ctttgggagg ctgaggtgga cagatcactt gaggtcagga
661  gtttgacacc agcctgggca gcatggcgaa acccgtctc tacaaaaaat acatatatat
721  tagccagatg tgggtgtgca tgctgtggt cccagcttct caggaagctg aggcaggaga
781  atcatttgaa cttgaggggc agaggttgca gtgagccaag attgtgccat ggaaccccaa
841  cctgggcaac agagcaagac tctgtctcaa aaaaaaaaaa aaatgctggc agtgggctgc
901  actttttttt ttcttaaaac ggaaaagggt taattatttc tttaaagaac ctagcaccaa
961  atacagtcac attcggaggt actggggggt gggacttgaa catatgaatt ttggaggggc
1021  acaaggcatc ccatgacaca tgtgggaacc ggtataatct ctacagagac tagaatttag
1081  atttaacagc ttgaaacagc ttcaagtatt tggtaacata caaaacaaaa acaattcaaa
1141  gcccttttaca ttcaaatatt tgaataaaaa ataactattt ctacaatgta taaaagggtat
1201  gctatgttta ttagtcttac ttgtagctaa tctactttta tgtttcctta cagaaaaattc
1261  ttgacatttt atgtttccgt gtaagagatt gtacagaagg caaatttttg tgttatgcaa
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Figure 24

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Figure 24

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SEQ ID NO: 10,476

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3067

Figure 25

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ctctttaatc	cttttaagcc	tcaatttctt	aattgtgaaa	tggggccta	acctgtatcc	300
aaccaaggga	gtagtttagaa	ggtaacatga	taggtggaaa	gcacttaaca	taggcaaaat	360
gttatkatca	ggaatgatcg	agagacccat	ccaactatct	gaaggagtca	cttaactcta	420
ctgtactgca	gcgctgtaaa	gtctgcatct	ttcactgggg	gtaaaggccc	ccagtccctg	480
agacggggca	gtttggagac	aggctgggtt	tttctctgtt	ctcctgagag	cccttcagat	540
gagaagggag	gtctggagac	agaatgccaa	aagcccatta	aaggcacggc	cttgcatttc	600
agagagggag	caggtctaga	gaagaaccag	aggagctcag	ctgagatatg	gtgtatggat	660
tggatttttg	tagaagatgg	gaagaaccaa	acacctgaga	aaccttttg	aagatcgggg	720
tcagagtaag	gcctaacaca	tagttggctc	ccagtaatta	ttggttgatt	gaacagctca	780
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gatttatatt	tattttatat	gtattttttc	tatttttttg	agacgaagty	tcactcactc	900
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aagcggtgtg	gaccggggcag	agggtgtatc	tgggactctg	ggttctcagc	ccggggacag	2160
cgaaccgagg	ggcagatgat	ccatcagaaa	agagccggca	ctgcccagcc	ccgcgcccct	2220
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tttgagcccg	gcccccaagct	ctgggacagt	cgtgcccctc	atcaagggaag	agccaaggac	2340
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cagcaataac	ttatttgtct	ttatccaaca	gccataaaat	ataactttaa	atattctatt	2820
gatagagaaa	ggagttcatg	aaggcagaaa	tgcttggggc	ccacgaacat	ccagtggtgg	2880
ccctggacgg	gacatcatgc	tgggcaacac	agctaaaaatg	cgggtgaaga	ccagatttct	2940
tgcacatggc	ggtgacggga	tgctccctag	agagcttcaa	gtggatttct	tgctttttat	3000
tttctctctt	aataaaaaatg	tatgatgttt	acattgtcag	agaaaaaaaa	aaaaaaaaaa	3060
ctcgtagggg	gggcccgtac	ccaatcgctt	gtgatgatgg	tatac		3105

Figure 26

10057475.012002

Ly1488 Protein Sequence (SERID NO: 10,969)

ELLKSIWYAFTALDVEKSGKVSQKLVLSHNLTYTLVLIHPHDPV
 ALEEHFRDDDDGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDLWCWTLTAKKNYRADS
 NGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEPVPSTKHPNKTQDP
 PESPKQSVKSCWGRLEWEPDRALPGVGAGNTTCCSYQAFLLLLQVEYLLKKVLSMSL
 EVSLGELEELLAQEAQVAQTGGLSVWQFLELFNSGRCLRGVGRDTLSMAIHEVYQEL
 IQDVLKQGYLWKRGLRRNWAERWFQLOPSCLCYFGSEECCKEKGIIPLDAHCCVEVL
 PDRDGKRCMFCVKTANRTYEMSASDTRQREWTAAIQMAIRLQAEKGTSLHKDLKQKR
 REQREQRERRRAAKEEELLRLQQLQEEKERKLQEELELLQEAQQAERLLQEEEEERRRS
 QHRELQQALEBGLREAEQARASMQAEMELKEEEAARQRIKELEEMQQRLOEALQLE
 VKARRDEESVRIAQTRLLEEEEEKLKQLMQLKEEQERYIERAQKEEELQOEMAQQR
 SLQQAQQQLLEEVQRQRADEDEVAQAQRKLQASTNVKHWNVQMNRLMHPTEPGDKRP
 VTSSSFSGFPPLLAHRDSSLKRLTRWGSQGNRTSPSPNSNEQQKSLNGGDEAPAPAST
 PQEDKLDPAEN"

Ly1488 DNA Sequence (mRNA) (SERID NO: 10,970)

1 gaactgctca agtccatctg gtacgccttt accgcgctgg acgtggagaa gagtggcaaa
 61 gtctccaagt cccagctcaa ggtgctgtcc cacaacctgt acacggtcct gcacatcccc
 121 catgaccccg tggccctgga ggaacacttc cgagatgatg atgacggccc tgtgtccagc
 181 cagggataca tggccctacct caacaagtac atccttgaca aggtggagga gggggctttt
 241 gttaaagagc actttgatga gctgtgctgg acgctgacgg ccaagaagaa ctatcgggga
 301 gatagcaacg ggaacagtat gctctccaat caggatgcct tccgcctctg gtgcctcttc
 361 aacttcctgt ctgaggacaa gtacctctg atcatggttc ctgatgaggg tgatgaaggg
 421 aaccaccgga gccctgaacc agtgccctct actaaacacc caaacaagac ccaggatccc
 481 ccagaaagtc ctaaacagag tgtcccaaaa agctgctggg gcaggctctg ggagccagat
 541 agagcactcc ctgggtgttg tgctggcaac accacctgct gcagctacca ggccttcctt
 601 ctccctgctcc aggttgaata cctgctgaaa aaggtactca gcagcatgag cttggagggtg
 661 agcttgggtg agctggagga gcttctggcc caggaggccc aggtggccca gaccaccggg
 721 gggctcagcg tctggcagtt cctggagctc ttcaattcgg gccgctgcct gcggggcggtg
 781 ggccgggaca ccctcagcat ggccatccac gaggtctacc aggagctcat ccaagatgtc
 841 ctgaagcagg gctacctgtg gaagcgaggg cacctgagaa ggaactgggc cgaacgctgg
 901 ttccagctgc agccagctg cctctgtac tttgggagtg aagagtgcaa agagaaaagg
 961 ggcattatcc cgctggatgc acactgctgc gtggagggtg tgccagaccg cgacggaaag
 1021 cgctgcatgt tctgtgtgaa gacagccaac cgcacgtatg agatgagcgc ctgagacacg
 1081 cgccagcgcc aggagtgagc agctgccatc cagatggcga tccggctgca ggccgagggg
 1141 aagacgtccc tacacaagga cctgaagcag aaacggcgcg agcagcgga gcagcgggag
 1201 cggcgccggg cggccaagga agaggagctg ctgcggtgca agcagctgca ggaggagaag
 1261 gagcgggaagc tgcaggagct ggagctgtg caggaggcgc agcggcaggc cgagcggtg
 1321 ctgcaggagg aggaggaacg gcggcgagc cagcaccgcg agctgcagca ggcgctcgag
 1381 ggccaactgc gcgaggcgga gcaggcccgg gcctccatgc aggtgagat ggagctgaag
 1441 gaggaggagg ctgcccggca gcggcagcgc atcaaggagc tggaggagat gcagcagcgg
 1501 ttgcaggagg ccctgcaact agagggtgaaa gctcggcgag atgaagaatc tgtgcgaatc
 1561 gctcagacca gactgctgga agaggaggaa gagaagctga agcagttgat gcagctgaag
 1621 gaggagcagg agcgctacat cgaacgggcg cagcaggaga aggaagagct gcagcaggag
 1681 atggcacagc agagccgctc cctgcagcag gccagcagc agctggagga ggtgcggcag
 1741 aaccggcaga gggctgacga ggatgtggag gctgccaga gaaaactgcg ccaggccagc
 1801 accaactgta aacactggaa tgtccagatg aaccggctga tgcattcaat tgagcctgga
 1861 gataagcgctc cggtcaccag cagctccttc tcaggcttcc agccccctct gcttgcccac
 1921 cgtgactcct ccctaaagcg cctgaccgct tggggatccc agggcaacag gacccccctg
 1981 cccaacagca atgagcagca gaagtccctc aatggtgggg atgaggctcc tgccccggct
 2041 tccacccctc aggaagataa actggatcca gcaccagaaa attagcctct cttagccct
 2101 tgttcttccc aatgtcatat ccaccaggac ctggccacag ctggcctgtg ggtgatccca
 2161 gctcttacta ggagagggag ctgaggtcct ggtgccaggg gccaggcccc tccaaccata
 2221 aacagtcagg gatggaacct ggttcaccct tcataccagc tccaagcccc agaccatggg
 2281 agctgtcttg gatgttgatc cttgagaact tggccctgtg ctttagaccc aaggaccgga
 2341 ttcttgggct aggaaagaga gaacaagcaa gccggggcta cctgccccca ggtggccacc
 2401 aagtgtgtga agcacatttc taaataaaaa ctgctcttag aatgaa

Figure 27

TMpred Report for Ly1488 (SEQUENCE: 10,969)

ELLKSIWYAFTALDVEKSGKVSQKVLSHNLYTVLHIPHDPVALEEHF
RDDDDGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDELCWTLTAKKNYRA
DSNGNSMLSNQDAFRLWCLFNFLSEDKYPLIMVPDEGDEGNHPSPEPVPS
TKHPNKTQDPPESPQSVPKSCWGRLWEPDRALPGVGAGNTTCCSYQAF
LLLQVEYLLKKVLSSMSLEVSLGELEELLAQEAQVAQTGGLSVWQFLEL
FNSGRCLRGVGRDTLSMAIHEVYQELIQDVLKQGYLWKRGLRRNWAERW
FQLQPSCLCYFGSEECKEKGIIPLDAHCCVEVLPDRDGKRCMFCVKTAN
RTYEMSASDTRQREQWTAAIQMAIRLQAEGKTSLHKDLKQKRREQREQRE
RRRAAKEEELLRLQQLQEEKERKLQELLELLQEAQRQAERLLQEEERRRS
QHRELQQALEGQLREAEQARASMQAEMELKEEEAARQRQRIKELEEMQQR
LQEALQLEVKARRDEESVRIAQTRLLEEEEEKLKQLMQLKEEQERYIERA
QQEKEELQQEMAQQSRSLQQAQQQLLEVRQNRQRADEDVEAAQRKLQAS
TNVKHWNVMNRLMHPPIEPGDKRPVTSSSFSGFPPLLAHRDSSLKRLTR
WGSQGNRTPSPNSNEQQKSLNGGDEAPAPASTPQEDKLDPAPE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 199 - 220 Score: 1.3061

Figure 28

20220504

Lyl449 and Lyl480 matches Lung cancer associated
polynucleotide sequence SEQ ID

10,476

cttaaagagg	taatttagcc	atcattctta	tgccagcaga	tataaataaa	cttggaccca	60
tctgggtcttc	agctaaacct	gagacatttt	aaagtgcata	gacagccatg	gacagcaggc	120
cctcctctaa	caggggatgc	aaggcatgga	gaaagacaat	cagtacccaa	gctcagccac	180
agaagacagg	agtcactcat	ataacttggt	tttagaagtt	tttggtagcc	acgcacactt	240
tctgaaatca	cactatctgg	tggtttaatc	atatttttaa	agacagaatc	cctgagtgct	300
gagcagattc	tcaaaaacaca	tttagaatcc	ctgaaattag	aaagatcaat	gacaaaatat	360
ctgtcagcca	ggccacaaac	aggtgtaaaa	ttatgaaagg	agtggttgga	tgtgccaaagt	420
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cacctatgta	ggaagtgcgt	ggagttttct	gtcttctttc	tgtgtgattt	ttggcctttt	600
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agctacattg	tgtcactgga	cattttttaa	aactgtgatt	tttaataaaa	atttaaaatt	1500
tgaaaaaaaaa	aaaaaaaaac	ctcgggggta	acttttrggg	gggccggggc	ccwtgcgctt	1560
t						1561

Figure 29

10057475.01202

Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)

(SEQ ID NO: 10,474)

1 tgtatgtatg tgtgtggtgt gtgaaggtgt atgtggtatg tgtttggtat gtgtatatgt
61 gtactgtgtg gtgcattgcat gttctgtgta tttgtgtgca tgtgtatgta tgtgtgcccc
121 tctctgcata tgtgtatgta tatgtgtgca tgtgggtaca ggtgtatgta catgcatgca
181 catgtgtgca catgtgtgaa tgcattgtgta catttgtgca tgtgcttatg tgtgtggatg
241 catgtgttca tgtaaatgca tgcatttgtg cccatgcaca tgtgtatgta catgtgtgca
301 tatacatgta tgcactgaca tatatgcatg tgtgcatatg tacacgtgtg catgacctct
361 gtgcatgtgt gaatgcatgt gtgcatgtgg atgtatatgt gtgcatgtct gcgcatgtgt
421 gtaacctcct tagaacaggc agaaattggg gctctggaat cctttctttg cctaccgcag
481 ttctcttttag gctgtcttca tagagaaagg gatagctcaa aaccacagc cctgctttgg
541 cctgatgggg gatttctggg tctcctcagt ctgtctttta ttaggcaggc catgggctgt
601 caggccctgg ctgggtagat gctctgctca tgaataaaag atagaggcag ggcaggacag
661 ggcctccct gatgggctc cccgccttc tgtgtggtg aatctcacag tcaactttga
721 cctgtgcaca tccacttttt tttttgagat aggatcttgc tctgtcacc agctgggagt
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841 cccagcctc ccaagtagct gggactacag gtgcatacca ccacacccgg ctaatgtttt
901 gatttctgca gagctaaagt ctactatgt tgtccaggct ggtctcaaac tctgggtcca
961 agagactctc ctgcttggg ctcccaact gctgggatta caggcatgag ccaactgcacc
1021 cggccaacac attcactttt ttgggacatg gcagggaact aatgttttag aaaacattta
1081 gctaccctct tgacaatgct gcttgacact atttgacagt gtgacttacc acatccta
1141 aacttccatg aaaatcatca caaagcaaat tttaaatttt tattaataat cacagttttt
1201 aaaaatgtcc agtgacacaa tgtagctctt ctgaaatgaa tggaaaacac aacacactgc
1261 taaccagtgg agggagctct ctgcagggtc gggagacctg acaatgcagc tgtagcctct
1321 gcaagtgaat atccaggccg acttgacatc attggactga tgtccaagt caatcaccat
1381 acagcagcta caggcagggc tggctgatag ggagtatggg agaaggacac gctcagatga
1441 aaacatgcat gcaacgattt tcaccactga acacactgtt ttctgtgata gaaactgtcg
1501 gcctgtctgg gggacaagat attcacggcc tcaactagcca gtgtgatgcc accagggcag
1561 cctgccccct atgctccttt gttacctgct aaagaaggac cataaggtaa aaggcacctt
1621 accttatggg gtgagccag accccaggga aaagcttggg tagaacaatc caaggggcag
1681 cctgggtatg agaatccagc ccaagctagc tgccttagaa gcctggaggc ctttccagc
1741 ttcccaaatg tagccctttt cacatgacca atccttcaat taggttacct ttctctattt
1801 gcctctctg gtggtctacg gggaaaggat aattattcct gaccacaaga cacattttca
1861 ctagaaaaag cttctctgtg tggccacag tgggaattct gcacacaggt gcctgtcca
1921 ccaagcagag aggcctcagg gattgtccag ggacaaggag acctggccgg acctctgcag
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2101 aaactccag cacttctac ataggtgcta ccgtattcct acgagcacgg ggcctgtgtt
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2221 tctcagatgc agtcaccact ttaccaaact tggcacatcc aaccactcct ttcataattt
2281 tacacctgtt tgtggcctgg ctgacagata tttgtcatt gatctttcta atttcaggga
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2401 taaaccacca gatagtgtga tttcagaaag tgtgcgtggc taccaaaaac ttctaaacac
2461 aagttatagt agtgactcct gcttctgtg gctgagcttg ggtactgatt gtctttctcc
2521 atgcttga tccctgttta gaggagggtc tgcgtgccat ggctgtccat gcactttaaa
2581 atgtctcagg tttagctgaa gaccagatgg gtccaaagtt atttatatct gctggcataa
2641 gaatgatggc taaattacct ctttaagttg tttttttgt tgtttgtttt gacagagtct
2701 cgtgtgatg cccaagctgg agtgacgtgg catgatcttg gctcactgag acctccgttt
2761 cctgggttca agcgattctc ctgcccagc ctcccagta gctgggacta cagacacatg
2821 ccaccatgcc cggctaattt ttgtattttt agtagagatg gggttttacc atattggcca
2881 ggctagtctc aaactcctta cctcaagtga tccaccgcc tcggcctcct aaagtgtga
2941 gatgtctctt taactttcaa gaggtacagc aaaactgaaa tcaatgggtg atgactctt
3001 aaagatcaa catgaagatg aggtattgtt aagaccagaa aatcattctc cgatcttgta
3061 tcttcaactc aaattcacac tccaaaaggc ctgtttgtgg tgaggctcag ggtctttggc
3121 ttgtctgaa ttaatacttt ctttgaaac tcttttagatg gctttgatcc ctgtgctgcc
3181 cccattgca gacacagaaa gcgacagggt attctggcgg caccctctct gtggaggaga
3241 gaaaggtgtg gaccacgttc agaggaggc agcctgaagc tgtcctcagt gagatgtgg
3301 gggatgggct tcttgccctc gctgtgcagc ctccatgcag ggctttattt accagtcacc
3361 aggtcttcaa gacagtctgc aggagagagg atttcagggg gaaagtaagc caagccaatt
3421 cattctcatg gtcccctttt atcacaaaca tgtaatgtct ccatctcata acagagacag
3481 caaaagcagt atccaggcct tttttttttt tctttctaac tttcctaac tggctacatg
3541 cttagaaact gcaactggtc aacttgattt tcttttttaa gctcctaaac atttttattg
3601 tcaggaaaagc ttttcagtg ccagggatca gtctcatggc cgtagaagca gccaaattcc
3661 tctgcttttg ctttcccttc agagtgacac tgcataaggc tcttgggca tttggaaaag
3721 gccgcttggg gtgagagtgc tctaggccac tctgcaatgt ccctggggcc gatgagtaac
3781 aaatgcaccc cgggacccag agaagtgga agacatgaaa gggatttggg aacagatcgt
3841 aaaaataacc tgtatgaaaa tcacacagac aagaaaaaaa acaaatccag ctagccctgt
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4021 gcagagggag gtggctgaca atcaattcct ctggatacat tttcctgtga ttgctcctgt

Figure 30
Page 1 of 3

4081 gatcaaaggc agccaccgac aggtgcgggg gcggttagtt caccacgtca tagtagtaat
 4141 tgcgcagccg cagttccact gctgcgaatc cgggcctgtt ttccacactg gaatgggaaga
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Detection of Ly 1448P specific serum antibodies in lymphoma patients

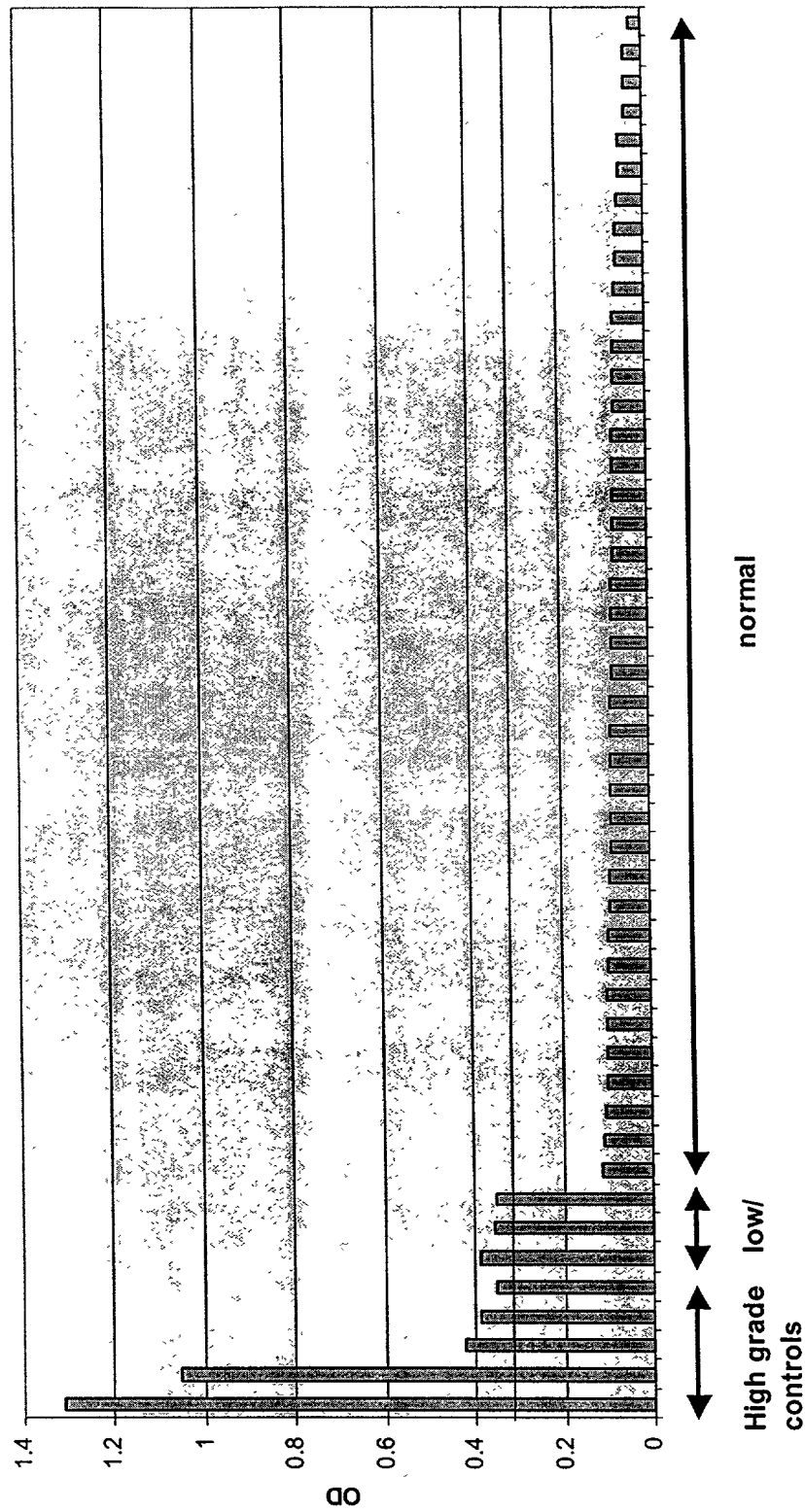


Figure 31

Detection of TCL-1 specific serum antibodies in lymphoma patients

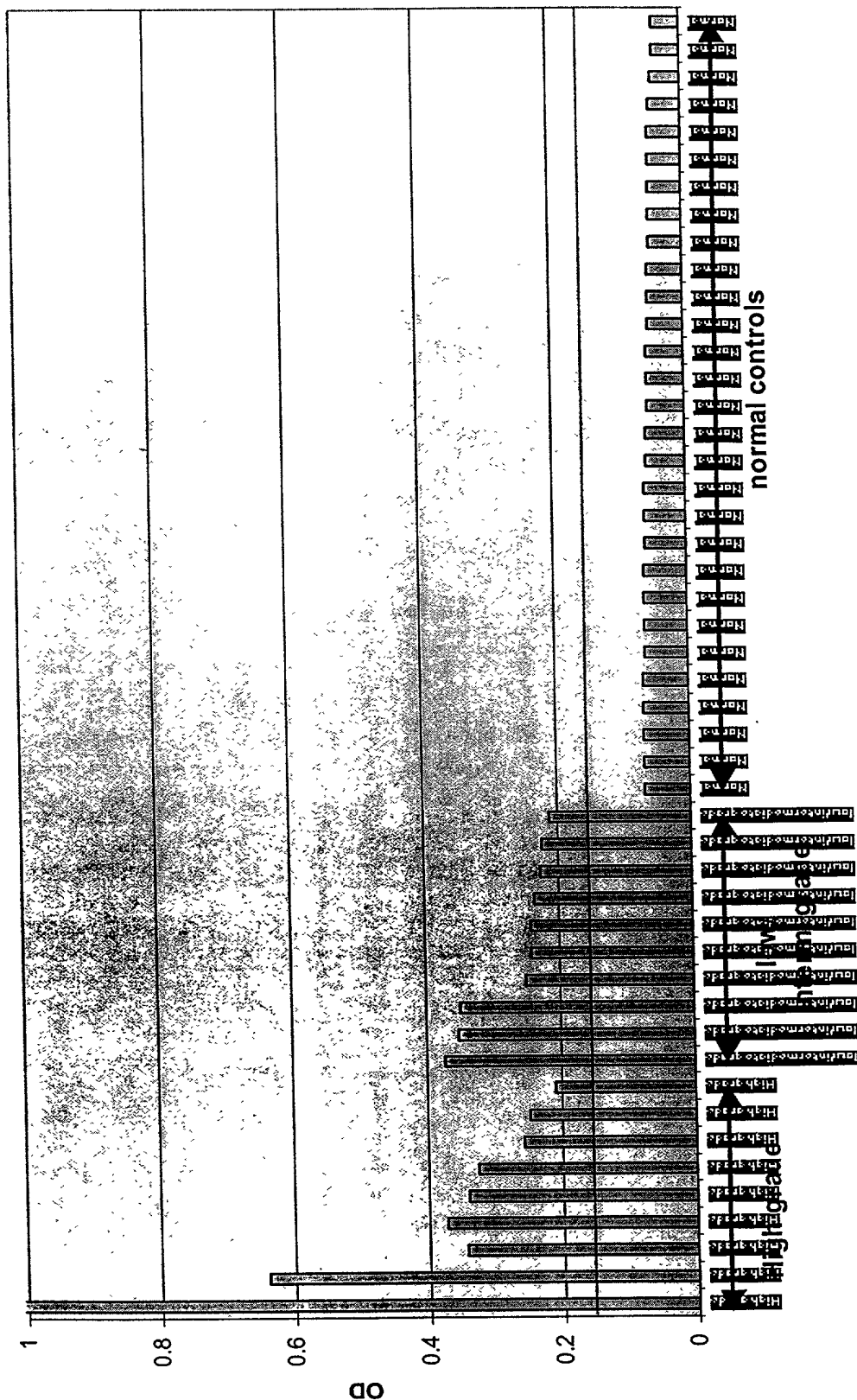


Figure 32